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OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/927,458

DATE: 08/23/2001

TIME: 14:53:08 ,

Input Set : A:\ES.txt

Output Set: N:\CRF3\08162001\I927458.raw

ENTERED

3 <110> APPLICANT: WALLACH, David

4 KOVALENKO, Andrei

6 <120> TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF RECEPTORS OF THE TNG/NGF
RECEPTOR FAMILY

7 AND OTHER PROTEINS

9 <130> FILE REFERENCE: WALLACH=22A

C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/927,458

12 <141> CURRENT FILING DATE: 2001-08-13

14 <150> PRIOR APPLICATION NUMBER: PCT/IL98/00125

15 <151> PRIOR FILING DATE: 1998-03-19

17 <150> PRIOR APPLICATION NUMBER: IL 120485

18 <151> PRIOR FILING DATE: 1997-03-19

20 <150> PRIOR APPLICATION NUMBER: 09/381,358

21 <151> PRIOR FILING DATE: 1999-09-20

23 <160> NUMBER OF SEQ ID NOS: 2

25 <170> SOFTWARE: PatentIn version 3.0

27 <210> SEQ ID NO: 1

28 <211> LENGTH: 2119

29 <212> TYPE: DNA

30 <213> ORGANISM: Homo sapiens

32 <220> FEATURE:

33 <221> NAME/KEY: CDS

34 <222> LOCATION: (217)..(1782)

36 <400> SEQUENCE: 1

37 tagggagacc caagcttctc gacggccatt accaatcgcg aaaccggcag ggcggccact 60

39 gtggcggggc tctttcccg tttcgctca gctaccctc agctccggtg gtcgccagtc 120

41 cggggtcgtc gccgtttggg gcgggagctg ctgcggcccg ccgccgtccc cgtcgccgct 180

43 tccgggtcca ggccctcgg gccgctgcc gccgtc atg agg ctg cgg gtg cgg 234

44 Met Arg Leu Arg Val Arg

45 1 5

47 ctt ctg aag cgg acc tgg ccg ctg gag gtg ccc gag acg gag ccg acg 282

48 Leu Leu Lys Arg Thr Trp Pro Leu Glu Val Pro Glu Thr Glu Pro Thr

49 10 15 20

51 ctg ggg cat ttg cgc tcg cac ctg agg ctg tcc ctg ctg tgc acc tgg 330

52 Leu Gly His Leu Arg Ser His Leu Arg Leu Ser Leu Leu Cys Thr Trp

53 25 30 35

55 ggg tac agt tct aat acc cga ttt aca att aca ttg aac tac aag gat 378

56 Gly Tyr Ser Ser Asn Thr Arg Phe Thr Ile Thr Leu Asn Tyr Lys Asp

57 40 45 50

59 ccc ctc act gga gat gaa gag acc ttg gct tca tat ggg att gtt tct 426

60 Pro Leu Thr Gly Asp Glu Glu Thr Leu Ala Ser Tyr Gly Ile Val Ser

61 55 60 65 70

63 ggg gac ttg ata tgt ttg att ctt caa gat gac att cca gcg cct aat 474

64 Gly Asp Leu Ile Cys Leu Ile Leu Gln Asp Asp Ile Pro Ala Pro Asn

65 75 80 85

67 ata cct tca tcc aca gat tca gag cat tct tca ctc cag aat aat gag 522

68 Ile Pro Ser Ser Thr Asp Ser Glu His Ser Ser Leu Gln Asn Asn Glu

69 90 95 100

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71	caa ccc tct ttg gcc acc agc tcc aat cag act agc atg cag gat gaa	570
72	Gln Pro Ser Leu Ala Thr Ser Ser Asn Gln Thr Ser Met Gln Asp Glu	
73	105 110 115	
75	caa cca agt gat tca ttc caa gga cag gca gcc cag tct ggt gtt tgg	618
76	Gln Pro Ser Asp Ser Phe Gln Gly Gln Ala Ala Gln Ser Gly Val Trp	
77	120 125 130	
79	aat gac gac agt atg tta ggg cct agt caa aat ttt gaa gct gag tca	666
80	Asn Asp Asp Ser Met Leu Gly Pro Ser Gln Asn Phe Glu Ala Glu Ser	
81	135 140 145 150	
83	att caa gat aat gcg cat atg gca gag ggc aca ggt ttc tat ccc tca	714
84	Ile Gln Asp Asn Ala His Met Ala Glu Gly Thr Gly Phe Tyr Pro Ser	
85	155 160 165	
87	gaa ccc atg ctc tgt agt gaa tcg gtg gaa ggg caa gtg cca cat tca	762
88	Glu Pro Met Leu Cys Ser Glu Ser Val Glu Gly Gln Val Pro His Ser	
89	170 175 180	
91	tta gag acc ttg tat caa tca gct gac tgt tct gat gcc aat gat gcc	810
92	Leu Glu Thr Leu Tyr Gln Ser Ala Asp Cys Ser Asp Ala Asn Asp Ala	
93	185 190 195	
95	ttg ata gtg ttg ata cat ctt ctc atg ttg gag tca ggt tac ata cct	858
96	Leu Ile Val Leu Ile His Leu Leu Met Leu Glu Ser Gly Tyr Ile Pro	
97	200 205 210	
99	cag ggc acc gaa gcc aaa gca ctg tcc atg ccg gag aag tgg aag ttg	906
100	Gln Gly Thr Glu Ala Lys Ala Leu Ser Met Pro Glu Lys Trp Lys Leu	
101	215 220 225 230	
103	agc ggg gtg tat aag ctg cag tac atg cat cct ctc tgc gag ggc agc	954
104	Ser Gly Val Tyr Lys Leu Gln Tyr Met His Pro Leu Cys Glu Gly Ser	
105	235 240 245	
107	tcc gct act ctc acc tgt gtg cct ttg gga aac ctg att gtt gta aat	1002
108	Ser Ala Thr Leu Thr Cys Val Pro Leu Gly Asn Leu Ile Val Val Asn	
109	250 255 260	
111	gct aca cta aaa atc aac aat gag att aga agt gtg 'aaa aga ttg cag	1050
112	Ala Thr Leu Lys Ile Asn Asn Glu Ile Arg Ser Val Lys Arg Leu Gln	
113	265 270 275	
115	ctg cta cca gaa tct ttt att tgc aaa gag aaa cta ggg gaa aat gta	1098
116	Leu Leu Pro Glu Ser Phe Ile Cys Lys Glu Lys Leu Gly Glu Asn Val	
117	280 285 290	
119	gcc aac ata tac aaa gat ctt cag aaa ctc tct cgc ctc ttt aaa gac	1146
120	Ala Asn Ile Tyr Lys Asp Leu Gln Lys Leu Ser Arg Leu Phe Lys Asp	
121	295 300 305 310	
123	cag ctg gtg tat cct ctt ctg gct ttt acc cga caa gca ctg aac cta	1194
124	Gln Leu Val Tyr Pro Leu Leu Ala Phe Thr Arg Gln Ala Leu Asn Leu	
125	315 320 325	
127	cca gat gta ttt ggg ttg gtc gtc ctc cca ttg gaa ctg aaa cta cgg	1242
128	Pro Asp Val Phe Gly Leu Val Val Leu Pro Leu Glu Leu Lys Leu Arg	
129	330 335 340	
131	atc ttc cga ctt ctg gat gtt cgt tcc gtc ttg tct ttg tct gcg gtt	1290
132	Ile Phe Arg Leu Leu Asp Val Arg Ser Val Leu Ser Leu Ser Ala Val	
133	345 350 355	
135	tgt cgt gac ctc ttt act gct tca aat gac cca ctc ctg tgg agg ttt	1338

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136 Cys Arg Asp Leu Phe Thr Ala Ser Asn Asp Pro Leu Leu Trp Arg Phe
137      360      365      370
139 tta tat ctg cgt gat ttt cga gac aat act gtc aga gtt caa gac aca      1386
140 Leu Tyr Leu Arg Asp Phe Arg Asp Asn Thr Val Arg Val Gln Asp Thr
141 375      380      385      390
143 gat tgg aaa gaa ctg tac agg aag agg cac ata caa aga aaa gaa tcc      1434
144 Asp Trp Lys Glu Leu Tyr Arg Lys Arg His Ile Gln Arg Lys Glu Ser
145      395      400      405
147 ccg aaa ggg cgg ttt gtg atg ctc ctg cca tcg tca act cac acc att      1482
148 Pro Lys Gly Arg Phe Val Met Leu Leu Pro Ser Ser Thr His Thr Ile
149      410      415      420
151 cca ttc tat ccc aac ccc ttg cac cct agg cca ttt cct agc tcc cgc      1530
152 Pro Phe Tyr Pro Asn Pro Leu His Pro Arg Pro Phe Pro Ser Ser Arg
153      425      430      435
155 ctt cct cca gga att atc ggg ggt gaa tat gac caa aga cca aca ctt      1578
156 Leu Pro Pro Gly Ile Ile Gly Gly Glu Tyr Asp Gln Arg Pro Thr Leu
157      440      445      450
159 ccc tat gtt gga gac cca atc agt tca ctc att cct ggt cct ggg gag      1626
160 Pro Tyr Val Gly Asp Pro Ile Ser Ser Leu Ile Pro Gly Pro Gly Glu
161 455      460      465      470
163 acg ccc agc cag ttt cct cca ctg aga cca cgc ttt gat cca gtt ggc      1674
164 Thr Pro Ser Gln Phe Pro Pro Leu Arg Pro Arg Phe Asp Pro Val Gly
165      475      480      485
167 cca ctt cca gga cct aac ccc atc ttg cca ggg cga ggc ggc ccc aat      1722
168 Pro Leu Pro Gly Pro Asn Pro Ile Leu Pro Gly Arg Gly Gly Pro Asn
169      490      495      500
171 gac aga ttt ccc ttt aga ccc agc agg ggt cgg cca act gat ggc cgg      1770
172 Asp Arg Phe Pro Phe Arg Pro Ser Arg Gly Arg Pro Thr Asp Gly Arg
173      505      510      515
175 ctg tca ttc atg tgattgattt gtaatttcat ttctggagct ccatttgatt      1822
176 Leu Ser Phe Met SV
177      520
179 ttgtttctaa actacagatg tcaactcett ggggtgctga tctcgagtgt tattttctga      1882
181 ttgtggtggt gagagttgca ctcccagaaa ccttttaaga gatacattta tagccctagg      1942
183 ggtggtatga cccaaagggt cctctgtgac aagggtggcc ttgggaatag ttggtgcca      2002
185 atctccctgc tcttggttct cctctagatt gaagtttggt ttctgatgct gttcttacca      2062
187 gattaaaaaa aagtgtaaat taaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa      2119
190 <210> SEQ ID NO: 2
191 <211> LENGTH: 522
192 <212> TYPE: PRT
193 <213> ORGANISM: Homo sapiens
195 <400> SEQUENCE: 2
197 Met Arg Leu Arg Val Arg Leu Leu Lys Arg Thr Trp Pro Leu Glu Val
198 1      5      10      15
201 Pro Glu Thr Glu Pro Thr Leu Gly His Leu Arg Ser His Leu Arg Leu
202      20      25      30
205 Ser Leu Leu Cys Thr Trp Gly Tyr Ser Ser Asn Thr Arg Phe Thr Ile
206      35      40      45
209 Thr Leu Asn Tyr Lys Asp Pro Leu Thr Gly Asp Glu Glu Thr Leu Ala

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210	50		55		60											
213	Ser	Tyr	Gly	Ile	Val	Ser	Gly	Asp	Leu	Ile	Cys	Leu	Ile	Leu	Gln	Asp
214	65					70					75				80	
217	Asp	Ile	Pro	Ala	Pro	Asn	Ile	Pro	Ser	Ser	Thr	Asp	Ser	Glu	His	Ser
218					85					90					95	
221	Ser	Leu	Gln	Asn	Asn	Glu	Gln	Pro	Ser	Leu	Ala	Thr	Ser	Ser	Asn	Gln
222				100					105					110		
225	Thr	Ser	Met	Gln	Asp	Glu	Gln	Pro	Ser	Asp	Ser	Phe	Gln	Gly	Gln	Ala
226			115					120					125			
229	Ala	Gln	Ser	Gly	Val	Trp	Asn	Asp	Asp	Ser	Met	Leu	Gly	Pro	Ser	Gln
230		130					135					140				
233	Asn	Phe	Glu	Ala	Glu	Ser	Ile	Gln	Asp	Asn	Ala	His	Met	Ala	Glu	Gly
234	145				150					155					160	
237	Thr	Gly	Phe	Tyr	Pro	Ser	Glu	Pro	Met	Leu	Cys	Ser	Glu	Ser	Val	Glu
238				165					170						175	
241	Gly	Gln	Val	Pro	His	Ser	Leu	Glu	Thr	Leu	Tyr	Gln	Ser	Ala	Asp	Cys
242			180						185					190		
245	Ser	Asp	Ala	Asn	Asp	Ala	Leu	Ile	Val	Leu	Ile	His	Leu	Leu	Met	Leu
246			195					200					205			
249	Glu	Ser	Gly	Tyr	Ile	Pro	Gln	Gly	Thr	Glu	Ala	Lys	Ala	Leu	Ser	Met
250		210					215					220				
253	Pro	Glu	Lys	Trp	Lys	Leu	Ser	Gly	Val	Tyr	Lys	Leu	Gln	Tyr	Met	His
254	225				230					235					240	
257	Pro	Leu	Cys	Glu	Gly	Ser	Ser	Ala	Thr	Leu	Thr	Cys	Val	Pro	Leu	Gly
258				245					250						255	
261	Asn	Leu	Ile	Val	Val	Asn	Ala	Thr	Leu	Lys	Ile	Asn	Asn	Glu	Ile	Arg
262			260					265						270		
265	Ser	Val	Lys	Arg	Leu	Gln	Leu	Leu	Pro	Glu	Ser	Phe	Ile	Cys	Lys	Glu
266			275					280					285			
269	Lys	Leu	Gly	Glu	Asn	Val	Ala	Asn	Ile	Tyr	Lys	Asp	Leu	Gln	Lys	Leu
270		290				295					300					
273	Ser	Arg	Leu	Phe	Lys	Asp	Gln	Leu	Val	Tyr	Pro	Leu	Leu	Ala	Phe	Thr
274	305				310					315						320
277	Arg	Gln	Ala	Leu	Asn	Leu	Pro	Asp	Val	Phe	Gly	Leu	Val	Val	Leu	Pro
278				325					330						335	
281	Leu	Glu	Leu	Lys	Leu	Arg	Ile	Phe	Arg	Leu	Leu	Asp	Val	Arg	Ser	Val
282			340					345					350			
285	Leu	Ser	Leu	Ser	Ala	Val	Cys	Arg	Asp	Leu	Phe	Thr	Ala	Ser	Asn	Asp
286			355					360					365			
289	Pro	Leu	Leu	Trp	Arg	Phe	Leu	Tyr	Leu	Arg	Asp	Phe	Arg	Asp	Asn	Thr
290		370				375					380					
293	Val	Arg	Val	Gln	Asp	Thr	Asp	Trp	Lys	Glu	Leu	Tyr	Arg	Lys	Arg	His
294	385				390					395					400	
297	Ile	Gln	Arg	Lys	Glu	Ser	Pro	Lys	Gly	Arg	Phe	Val	Met	Leu	Leu	Pro
298				405					410						415	
301	Ser	Ser	Thr	His	Thr	Ile	Pro	Phe	Tyr	Pro	Asn	Pro	Leu	His	Pro	Arg
302			420					425					430			
305	Pro	Phe	Pro	Ser	Ser	Arg	Leu	Pro	Pro	Gly	Ile	Ile	Gly	Gly	Glu	Tyr
306			435				440						445			

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309 Asp Gln Arg Pro Thr Leu Pro Tyr Val Gly Asp Pro Ile Ser Ser Leu
310      450                      455                      460
313 Ile Pro Gly Pro Gly Glu Thr Pro Ser Gln Phe Pro Pro Leu Arg Pro
314 465                      470                      475                      480
317 Arg Phe Asp Pro Val Gly Pro Leu Pro Gly Pro Asn Pro Ile Leu Pro
318                      485                      490                      495
321 Gly Arg Gly Gly Pro Asn Asp Arg Phe Pro Phe Arg Pro Ser Arg Gly
322                      500                      505                      510
325 Arg Pro Thr Asp Gly Arg Leu Ser Phe Met
326                      515                      520
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VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number